

#6
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TECH CENTER 1600/2900

SEQUENCE LISTING

<110> Kapeller-Libermann, Rosana

<120> 58860, A HUMAN CHOLESTERYL ESTER
HYDROLASE AND USES THEREFOR

<130> MPI2001-026P1RNM

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<141> 2002-01-25

<150> 60/264,167

<151> 2001-01-25

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tgt	gga	act	tta	aat	gct	ggt	gga	ttc	ctt	gat	ttg	gaa	aat	gaa	gtg	99
Cys	Gly	Thr	Leu	Asn	Ala	Gly	Gly	Phe	Leu	Asp	Leu	Glu	Asn	Glu	Val	
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aat	cct	gag	gtg	tgg	atg	aat	act	agt	gaa	atc	atc	atc	tac	aat	ggc	147
Asn	Pro	Glu	Val	Trp	Met	Asn	Thr	Ser	Glu	Ile	Ile	Ile	Tyr	Asn	Gly	
		30				35						40				

tac	ccc	agt	gaa	gag	tat	gaa	gtc	acc	act	gaa	gat	ggg	tat	ata	ctc	195
Tyr	Pro	Ser	Glu	Glu	Tyr	Glu	Val	Thr	Thr	Glu	Asp	Gly	Tyr	Ile	Leu	
		45				50				55					60	

ctt	gtc	aac	aga	att	cct	tat	ggg	cga	aca	cat	gct	agg	agc	aca	ggt	243
Leu	Val	Asn	Arg	Ile	Pro	Tyr	Gly	Arg	Thr	His	Ala	Arg	Ser	Thr	Gly	
			65					70						75		

ccc	cgg	cca	gtt	gtg	tat	atg	cag	cat	gcc	ctg	ttt	gca	gac	aat	gcc	291
Pro	Arg	Pro	Val	Val	Tyr	Met	Gln	His	Ala	Leu	Phe	Ala	Asp	Asn	Ala	
			80					85					90			

tac	tgg	ctt	gag	aat	tat	gct	aat	gga	agc	ctt	gga	ttc	ctt	cta	gca	339
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Tyr Trp Leu Glu Asn Tyr Ala Asn Gly Ser Leu Gly Phe Leu Leu Ala	
95 100 105	
gat gca ggt tat gat gta tgg atg gga aac agt cgg gga aac act tgg	387
Asp Ala Gly Tyr Asp Val Trp Met Gly Asn Ser Arg Gly Asn Thr Trp	
110 115 120	
tca aga aga cac aaa aca ctc tca gag aca gat gag aaa ttc tgg gcc	435
Ser Arg Arg His Lys Thr Leu Ser Glu Thr Asp Glu Lys Phe Trp Ala	
125 130 135 140	
ttt agt ttt gat gaa atg gcc aaa tat gat ctc cca gga gta ata gac	483
Phe Ser Phe Asp Glu Met Ala Lys Tyr Asp Leu Pro Gly Val Ile Asp	
145 150 155	
ttc att gta aat aaa act ggt cag gag aaa ttg tat ttc att gga cat	531
Phe Ile Val Asn Lys Thr Gly Gln Glu Lys Leu Tyr Phe Ile Gly His	
160 165 170	
tca ctt ggc act aca ata ggg ttt gta gcc ttt tcc acc atg cct gaa	579
Ser Leu Gly Thr Thr Ile Gly Phe Val Ala Phe Ser Thr Met Pro Glu	
175 180 185	
ctg gca caa aga atc aaa atg aat ttt gcc ttg ggt cct acg atc tca	627
Leu Ala Gln Arg Ile Lys Met Asn Phe Ala Leu Gly Pro Thr Ile Ser	
190 195 200	
ttc aaa tat ccc acg ggc att ttt acc agg ttt ttt cta ctt cca aat	675
Phe Lys Tyr Pro Thr Gly Ile Phe Thr Arg Phe Phe Leu Leu Pro Asn	
205 210 215 220	
tcc ata atc aag gct gtt ttt ggt acc aaa ggt ttc ttt tta gaa gat	723
Ser Ile Ile Lys Ala Val Phe Gly Thr Lys Gly Phe Phe Leu Glu Asp	
225 230 235	
aag aaa acg aag ata gct tct acc aaa atc tgc aac aat aag ata ctc	771
Lys Lys Thr Lys Ile Ala Ser Thr Lys Ile Cys Asn Asn Lys Ile Leu	
240 245 250	
tgg ttg ata tgt agc gaa ttt atg tcc tta tgg gct gga tcc aac aag	819
Trp Leu Ile Cys Ser Glu Phe Met Ser Leu Trp Ala Gly Ser Asn Lys	
255 260 265	
aaa aat atg aat cag agt cga atg gat gtg tat atg tca cat gct ccc	867
Lys Asn Met Asn Gln Ser Arg Met Asp Val Tyr Met Ser His Ala Pro	
270 275 280	
act ggt tca tca gta cac aac att ctg cat ata aaa cag ctt tac cac	915
Thr Gly Ser Ser Val His Asn Ile Leu His Ile Lys Gln Leu Tyr His	
285 290 295 300	
tct gat gaa ttc aga gct tat gac tgg gga aat gac gct gat aat atg	963
Ser Asp Glu Phe Arg Ala Tyr Asp Trp Gly Asn Asp Ala Asp Asn Met	
305 310 315	
aaa cat tac aat cag agt cat ccc cct ata tat gac ctg act gcc atg	1011
Lys His Tyr Asn Gln Ser His Pro Pro Ile Tyr Asp Leu Thr Ala Met	

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aaa gtg cct act gct att tgg gct ggt gga cat gat gtc ctc gta aca			1059
Lys Val Pro Thr Ala Ile Trp Ala Gly Gly His Asp Val Leu Val Thr			
335	340	345	
ccc cag gat gtg gcc agg ata ctc cct caa atc aag agt ctt cat tac			1107
Pro Gln Asp Val Ala Arg Ile Leu Pro Gln Ile Lys Ser Leu His Tyr			
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ttt aag cta ttg cca gat tgg aac cac ttt gat ttt gtc tgg ggc ctc			1155
Phe Lys Leu Leu Pro Asp Trp Asn His Phe Asp Phe Val Trp Gly Leu			
365	370	375	380
gat gcc cct caa cgg atg tac agt gaa atc ata gct tta atg aag gca			1203
Asp Ala Pro Gln Arg Met Tyr Ser Glu Ile Ile Ala Leu Met Lys Ala			
385	390	395	
tat tcc taa atggaaaaaa aaaaaaaaaa aaaaaaaaaa aaagcggccg			1252
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cggccgctaa att			1325
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Trp Met Asn Thr Ser Glu Ile Ile Ile Tyr Asn Gly Tyr Pro Ser Glu			
35 40 45			
Glu Tyr Glu Val Thr Thr Glu Asp Gly Tyr Ile Leu Leu Val Asn Arg			
50 55 60			
Ile Pro Tyr Gly Arg Thr His Ala Arg Ser Thr Gly Pro Arg Pro Val			
65 70 75 80			
Val Tyr Met Gln His Ala Leu Phe Ala Asp Asn Ala Tyr Trp Leu Glu			
85 90 95			
Asn Tyr Ala Asn Gly Ser Leu Gly Phe Leu Leu Ala Asp Ala Gly Tyr			
100 105 110			
Asp Val Trp Met Gly Asn Ser Arg Gly Asn Thr Trp Ser Arg Arg His			
115 120 125			
Lys Thr Leu Ser Glu Thr Asp Glu Lys Phe Trp Ala Phe Ser Phe Asp			
130 135 140			
Glu Met Ala Lys Tyr Asp Leu Pro Gly Val Ile Asp Phe Ile Val Asn			
145 150 155 160			
Lys Thr Gly Gln Glu Lys Leu Tyr Phe Ile Gly His Ser Leu Gly Thr			
165 170 175			
Thr Ile Gly Phe Val Ala Phe Ser Thr Met Pro Glu Leu Ala Gln Arg			
180 185 190			
Ile Lys Met Asn Phe Ala Leu Gly Pro Thr Ile Ser Phe Lys Tyr Pro			
195 200 205			
Thr Gly Ile Phe Thr Arg Phe Phe Leu Leu Pro Asn Ser Ile Ile Lys			

210	215	220
Ala Val Phe Gly Thr Lys Gly Phe Phe Leu Glu Asp Lys Lys Thr Lys		
225	230	235
Ile Ala Ser Thr Lys Ile Cys Asn Asn Lys Ile Leu Trp Leu Ile Cys		240
	245	250
Ser Glu Phe Met Ser Leu Trp Ala Gly Ser Asn Lys Lys Asn Met Asn		255
	260	265
Gln Ser Arg Met Asp Val Tyr Met Ser His Ala Pro Thr Gly Ser Ser		270
	275	280
Val His Asn Ile Leu His Ile Lys Gln Leu Tyr His Ser Asp Glu Phe		285
	290	295
Arg Ala Tyr Asp Trp Gly Asn Asp Ala Asp Asn Met Lys His Tyr Asn		300
305	310	315
Gln Ser His Pro Pro Ile Tyr Asp Leu Thr Ala Met Lys Val Pro Thr		320
	325	330
Ala Ile Trp Ala Gly Gly His Asp Val Leu Val Thr Pro Gln Asp Val		335
	340	345
Ala Arg Ile Leu Pro Gln Ile Lys Ser Leu His Tyr Phe Lys Leu Leu		350
	355	360
Pro Asp Trp Asn His Phe Asp Phe Val Trp Gly Leu Asp Ala Pro Gln		365
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Arg Met Tyr Ser Glu Ile Ile Ala Leu Met Lys Ala Tyr Ser		380
385	390	395

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Asn Ala Gly Gly Phe Leu Asp Leu Glu Asn Glu Val Asn Pro Glu Val	
20 25 30	
tgg atg aat act agt gaa atc atc atc tac aat ggc tac ccc agt gaa	144
Trp Met Asn Thr Ser Glu Ile Ile Ile Tyr Asn Gly Tyr Pro Ser Glu	
35 40 45	
gag tat gaa gtc acc act gaa gat ggg tat ata ctc ctt gtc aac aga	192
Glu Tyr Glu Val Thr Thr Glu Asp Gly Tyr Ile Leu Leu Val Asn Arg	
50 55 60	
att cct tat ggg cga aca cat gct agg agc aca ggt ccc cgg cca gtt	240
Ile Pro Tyr Gly Arg Thr His Ala Arg Ser Thr Gly Pro Arg Pro Val	
65 70 75 80	
gtg tat atg cag cat gcc ctg ttt gca gac aat gcc tac tgg ctt gag	288
Val Tyr Met Gln His Ala Leu Phe Ala Asp Asn Ala Tyr Trp Leu Glu	
85 90 95	

aat tat gct aat gga agc ctt gga ttc ctt cta gca gat gca ggt tat	336
Asn Tyr Ala Asn Gly Ser Leu Gly Phe Leu Leu Ala Asp Ala Gly Tyr	
100 105 110	
gat gta tgg atg gga aac agt cgg gga aac act tgg tca aga aga cac	384
Asp Val Trp Met Gly Asn Ser Arg Gly Asn Thr Trp Ser Arg Arg His	
115 120 125	
aaa aca ctc tca gag aca gat gag aaa ttc tgg gcc ttt agt ttt gat	432
Lys Thr Leu Ser Glu Thr Asp Glu Lys Phe Trp Ala Phe Ser Phe Asp	
130 135 140	
gaa atg gcc aaa tat gat ctc cca gga gta ata gac ttc att gta aat	480
Glu Met Ala Lys Tyr Asp Leu Pro Gly Val Ile Asp Phe Ile Val Asn	
145 150 155 160	
aaa act ggt cag gag aaa ttg tat ttc att gga cat tca ctt ggc act	528
Lys Thr Gly Gln Glu Lys Leu Tyr Phe Ile Gly His Ser Leu Gly Thr	
165 170 175	
aca ata ggg ttt gta gcc ttt tcc acc atg cct gaa ctg gca caa aga	576
Thr Ile Gly Phe Val Ala Phe Ser Thr Met Pro Glu Leu Ala Gln Arg	
180 185 190	
atc aaa atg aat ttt gcc ttg ggt cct acg atc tca ttc aaa tat ccc	624
Ile Lys Met Asn Phe Ala Leu Gly Pro Thr Ile Ser Phe Lys Tyr Pro	
195 200 205	
acg ggc att ttt acc agg ttt ttt cta ctt cca aat tcc ata atc aag	672
Thr Gly Ile Phe Thr Arg Phe Phe Leu Leu Pro Asn Ser Ile Ile Lys	
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gct gtt ttt ggt acc aaa ggt ttc ttt tta gaa gat aag aaa acg aag	720
Ala Val Phe Gly Thr Lys Gly Phe Phe Leu Glu Asp Lys Lys Thr Lys	
225 230 235 240	
ata gct tct acc aaa atc tgc aac aat aag ata ctc tgg ttg ata tgt	768
Ile Ala Ser Thr Lys Ile Cys Asn Asn Lys Ile Leu Trp Leu Ile Cys	
245 250 255	
agc gaa ttt atg tcc tta tgg gct gga tcc aac aag aaa aat atg aat	816
Ser Glu Phe Met Ser Leu Trp Ala Gly Ser Asn Lys Lys Asn Met Asn	
260 265 270	
cag agt cga atg gat gtg tat atg tca cat gct ccc act ggt tca tca	864
Gln Ser Arg Met Asp Val Tyr Met Ser His Ala Pro Thr Gly Ser Ser	
275 280 285	
gta cac aac att ctg cat ata aaa cag ctt tac cac tct gat gaa ttc	912
Val His Asn Ile Leu His Ile Lys Gln Leu Tyr His Ser Asp Glu Phe	
290 295 300	
aga gct tat gac tgg gga aat gac gct gat aat atg aaa cat tac aat	960
Arg Ala Tyr Asp Trp Gly Asn Asp Ala Asp Asn Met Lys His Tyr Asn	
305 310 315 320	

cag agt cat ccc cct ata tat gac ctg act gcc atg aaa gtg cct act 1008
 Gln Ser His Pro Pro Ile Tyr Asp Leu Thr Ala Met Lys Val Pro Thr
 325 330 335

gct att tgg gct ggt gga cat gat gtc ctc gta aca ccc cag gat gtg 1056
 Ala Ile Trp Ala Gly Gly His Asp Val Leu Val Thr Pro Gln Asp Val
 340 345 350

gcc agg ata ctc cct caa atc aag agt ctt cat tac ttt aag cta ttg 1104
 Ala Arg Ile Leu Pro Gln Ile Lys Ser Leu His Tyr Phe Lys Leu Leu
 355 360 365

cca gat tgg aac cac ttt gat ttt gtc tgg ggc ctc gat gcc cct caa 1152
 Pro Asp Trp Asn His Phe Asp Phe Val Trp Gly Leu Asp Ala Pro Gln
 370 375 380

cgg atg tac agt gaa atc ata gct tta atg aag gca tat tcc 1194
 Arg Met Tyr Ser Glu Ile Ile Ala Leu Met Lys Ala Tyr Ser
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 35 40 45
 Gly His Ser Met Gly Gly Ala Leu Ala Ala Ala Tyr Ala Ala Lys Tyr
 50 55 60
 Pro Glu Glu Arg Val Lys Ala Leu Val Leu Val Ser Thr Pro Ala Pro
 65 70 75 80
 Ala Gly Leu Ser Ser Arg Leu Phe Pro Arg Leu Gly Asn Leu Glu Gly
 85 90 95
 Leu Leu Leu Ala Asn Phe Phe Asn Arg Leu Ser Arg Ser Val Glu Ala
 100 105 110
 Leu Leu Gly Arg Ala Leu Lys Gln Phe Phe Leu Leu Gly Arg Pro Phe
 115 120 125
 Val Ser Asp Phe Leu Lys Gln Ala Glu Asp Trp Leu Ser Ser Leu Ala
 130 135 140
 Arg Pro Gly Glu Thr Asp Gly Gly Asp Gly Leu Gly Tyr Ala Val
 145 150 155 160
 Ala Leu Gly Lys Leu Leu Gln Trp Asp Arg Ser Ala Leu Lys Asp Ile
 165 170 175
 Lys Val Pro Thr Leu Val Ile Trp Gly Asp Asp Asp Pro Leu Val Pro
 180 185 190
 Leu Lys Ala Ser Glu Lys Leu Ser Ala Leu Phe Pro Asn Ala Glu Val
 195 200 205
 Val Val Ile Asp Asp Ala Gly His Leu Ala Leu Leu Glu Lys Pro Glu
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 Glu Val Ala Glu Leu Ile Lys Phe Leu
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          20           25           30
Arg Lys His Val Lys Leu Asn Pro Ser His Ser Glu Phe Trp Asp Phe
      35           40           45
Ser Trp His Glu Met Gly Met Tyr Asp Leu Pro Ala Met Ile Asp Tyr
      50           55           60
Val Leu Glu Thr Thr Gly Gln Glu Lys Leu His Tyr Val Gly His Ser
      65           70           75           80
Gln Gly Thr Thr Val Phe Phe Val Met Leu Ser Glu Arg Pro Glu Tyr
          85           90           95
Asn Glu Lys Ile Lys Ser Phe His Ala Leu Ala Pro Val Ala Tyr Met
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<223> The amino acid at position 2 can be any amino acid

<221> VARIANT
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<221> VARIANT
 <222> (4)...(4)
 <223> Xaa = L, I, V, M, S or T

<221> VARIANT
 <222> (6)...(6)
 <223> Xaa = H, Y, W or V

<223> The amino acid at position 8
 can be any amino acid

<221> VARIANT
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